

株日本触媒 基盤技術研究所 仙波 尚

Amino acid seq.
Cassava 由来 SHNL のアミノ酸配列(Gene Bank No. AJ223281)

MAVVDFVLIHTICHCAWIWYKLKPVLEAAGHKVTALDLAASGVDPHQIEQINSFDEYSEPLLTFMESLPQ
GEKVILVGESECGGLNIAJAADKYPEKIAAAVFQNSLLPDTKIIKPSYVVDKLMEVFPDWKDTYEFEFSNSN
GETITGMVLGLKLMRENLYTICPPEDYELAKMLTRRGSLFQSILAQREKFTEKGYGSIKKIYVWTGDDKI
FLPEFQLWQIENYKPDLVFRVMGGDIHKLQLTKTNEIAGILQKVADIYA

Amino acid seq.
Prunus 由来 RHNL のアミノ酸配列(Gene Bank No. AF043186)

MEKSTMSAVVLVLNLLVLHLQYSEVHSLANTSSEHDFGYLKFWYNAVDLELEGSYDYIIVGGGTSGCPLA
ATLSANYSVLVLERGTIATEYPNTLTVDCFAYNLQQQDDGKTPVERFVSEDGIDNVRSRILGGTTIINAGV
YARANESFYNNNSGVEWDLNLVNEAYEWVEDAIVYKPSNQSWQSITGTAFLFLEAGVHPDNGFGLVHEEGT
RLTCSTFDNSGTRHASDELLNKGDPDNLKVAVEAAVQKIIIFSTESSGLTAVGVVYTDNSNGTSHRALVSGK
GEVILSAGTLGTPQLLLSGVGPESYLTSLNISVVAHPYVCQYVNDNPRNFINILPPNPIEPSTVTVLGITS
DFYQCSLSSLPDTTPFSLFPTTSYPLPNQTFAHIVSKVPGPLSAGSLTLQSSNVSVAPNVKFNYCSDPV
DLTHCVSGMKKIGVFLSTDALKPYKVDDLPGIDGFNILGTPLPENQTDDAAFEKFCRDTVASYWHYHGG
AIVGKVIDGNFRVTGINALRVVDGSTFPATPASHPQGFYLMGRYVGTKIVQERSASGEAJHTSTFKPKLM
DSLKSALSFAF

両者のホモジニティ検索結果

[GENETYX : Maximum Matching]

Date : 2002.12.17

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Sequence 1 : M.esculenta SHNL AA seq

Size : 258

Matching Position : 1 - 258

Sequence 2 : P.serotina RHNL AA seq

Size : 574

Matching Position : 1 - 574

Matching Condition.

Matches	:	-1
Mismatches	:	1
Gaps	:	1
*N+	:	2

Matching : 15.68 [%]
Weight : 456

1 : M-----AVV -DFVL--IHT ICH----- --GAWIWYKL KPV----- LE-----
 * *** * * * * * **
1 : MEKSTMSAVV LVLNLVLHL QYSEVHSLAN TSSEHDFGYL KFVYNAVDLE LEGSYDYIIV

28 : -----AA-----GHKVT----- ALDLAASGVDF PROIEQINSF
* * * * *
61 : GGGTSGCPLA ATLSANYSVI VLERGTIAVE YPNTLTVDGF AYNLQQQDDG KTPVERFVSE

55 : D----EYSEP L----- --LTFMESLP QGEKV---I LVGESCGGLN IAI-----
* * * * * * * *
121 : DGIDNVRSRIGGGTTIINAG VYARANESFY NNSGVEWDD LVNEAYEWWE DAIIVYKPSNQ

89 : ----- AADKYPEKI AAAV ----- FQNS ----- LL ----- PD -----
* * * * * * * *
181 : SWOSITGTAF LEAGVHPDNG FGLVHBEGTR LTGSTFDNSG TRHASDELLN KGDPDNLKVA

152 : -----KLMREN LYТИCPPEDY E-----

* * * *

301 : GPESYLTSLN ISVVASHPYV GQYVNDNPRN FINILPPNPI EPSTVTVLGI TSDFYQCSLS

169 : LAKMLTRRGS LF-----QS---IL AQREKF---

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361 : SLPFDTPPFS LFPTTSYPLP NQTFAHIVSK VPGPLSAGSL TIQSSSNVSV APNVKFNYCS

191 : -----TEKGY GSIK----- KIYV-- WTGDD--- KIFLPEFQ-----

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421 : DPVDLTHCVS GMKKIGVFLS TDALKPYKVD DLPGIDGFNI LGTPLPENQT DDAAFEKFCR

217 : -----LWQIENYKPD LVFRVMG--- -----GDH KLQL----T

* * *** *

* * *

481 : DTVASYWHYH GGAIVGKVID GNFRVTGINA LRVVDGSTFP ATPASHPQGF YLMLGRYVGT

242 : K-----TNEIAG IL---QKVAD IYA-

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541 : KIVQERSASG EAIHTSTFKP KLMDSLKSAL SFAF

[GENETYX : Amino Acid Sequence Homology Data]

Date : 2002.12.17

1st Amino Acid Sequence

File Name : Cassava SHNL AA seq.
Sequence Size : 258

2nd Amino Acid Sequence

File Name : P.serotina RHNL AA seq
Sequence Size : 574

Unit Size to Compare = 2

Pick up Location = 1

[31.818% / 22 aa] INT/OPT.Score : < 21/ 63 >

1' MAVVDFVLIH TICHGAWIWy KLKPVLAAAG HKVTALDLAA SGVDPROIEQ INSFDEYSEP

1" MEKS TMSAVVLVLN LLVLHLQYSE

61' LLTFMESLPQ GEKVILVGES CGGLNIAIAA DKYPEKIAAA VFQNSLLPDT KHKPSYVVDK

25" VHSLANTSSE HDFGYLKFWY NAVDLELEGS YDYIIVGGGT SGCPLAATLS ANYSVLVLER

121' LMEVFPDWKD TEYFEFSNSN GETITGMVLG LKLMRENLYT ICPPEDYELA KMLTRRGSLF

85" GTIATEYPNT LTVDGFAYNL QQQDDGKTPV ERFVSEDGID NVRSRILGGT TIINAGVYAR

181' QSILAQREKF TEKGYGSIKK IYVWTGDDKI FLPEFQLWQI ENYKPDLVFR VMGGDHKLQL

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145" ANESFYNNNSG VEWDLDLVNE AYEWVEDAIV YKPSNQSWQS ITGTAFLLEAG VHPDNGFGLV

241' TKTNEIAGIL QKVADIYA

205" HEEGTRLTGS TFDNSGTRHA SDELLNKGD P DNLKVAVEAA VQKIIIFSTES SGLTAVGVVY